



-48-

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Jiang, Min
Potter, Andrew A.
MacLachlan, Philip R.

(ii) TITLE OF INVENTION: CAMP FACTOR OF STREPTOCOCCUS UBERIS

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Reed & Robins LLP
(B) STREET: 285 Hamilton Avenue, Suite 200
(C) CITY: Palo Alto
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94301

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/658,277
(B) FILING DATE: 05-JUN-1996
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Robins, Roberta L.
(B) REGISTRATION NUMBER: 33,208
(C) REFERENCE/DOCKET NUMBER: 9000-0030

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (415) 327-3400
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1191 base pairs

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 157..924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AATGAAACATA AAATAAAAAT TAATAATTAT ATATTTTAT GATAATCACA TATATTTGAC	60
TTAAAAAAAT TGTTACTGTA TGATACAGGC ATAAGTACTT ATTTATTTA TAGATTGCAA	120
TTTATAAACCA ATTATATTTT TCAAAGAGGA ATGCTT ATG GAA TTC AAA AAG TTA Met Glu Phe Lys Lys Leu	174
1 5	
CTT TAT TTA ACT GGT TCA ATC GCA GGA ATT ACT TTA TTT TCC CCA ATT Leu Tyr Leu Thr Gly Ser Ile Ala Gly Ile Thr Leu Phe Ser Pro Ile	222
10 15 20	
TTA ACA AGT GTC CAA GCA AAT CAA ATA AAT GTT AGT CAA CCA TCT AAT Leu Thr Ser Val Gln Ala Asn Gln Ile Asn Val Ser Gln Pro Ser Asn	270
25 30 35	
AAT GAA AGT AAT GTT ATT TCA CAG AAA AAA GAA GAA ATT GAT AAT AGT Asn Glu Ser Asn Val Ile Ser Gln Lys Lys Glu Glu Ile Asp Asn Ser	318
40 45 50	
CTA AAT CAG GAA AGT GCT CAA CTA TAT GCC TTG AAA GAA GAT GTT AAA Leu Asn Gln Glu Ser Ala Gln Leu Tyr Ala Leu Lys Glu Asp Val Lys	366
55 60 65 70	
GGA ACT GAG AAA GAA CAA TCA GTT AAT TCA GCA ATT TCA GCT GTT GAA Gly Thr Glu Lys Glu Gln Ser Val Asn Ser Ala Ile Ser Ala Val Glu	414
75 80 85	
AAT TTA AAA ACT TCA CTT AGA GCT AAT CCT GAA ACA ATT TAT GAT TTA Asn Leu Lys Thr Ser Leu Arg Ala Asn Pro Glu Thr Ile Tyr Asp Leu	462
90 95 100	
AAT TCG ATT GGA ACA AGA GTA GAA GCA ATC TCT GAC GTG ATT CAA GCA Asn Ser Ile Gly Thr Arg Val Glu Ala Ile Ser Asp Val Ile Gln Ala	510
105 110 115	
ATT GTT TTT TCA ACG CAA CAG TTA ACA AAT AAA GTT GAT CAA GCT CAC Ile Val Phe Ser Thr Gln Gln Leu Thr Asn Lys Val Asp Gln Ala His	558
135 140 145 150	

CCA TTT GCT TCA AAT GAA TCC ATT AAA GGG CAA GTC GAA GCT GTT AAA	654
Pro Phe Ala Ser Asn Glu Ser Ile Lys Gly Gln Val Glu Ala Val Lys	
155 160 165	
CAA GTG CAA GCG ACT GTG CTT ACC TAT CCC GAT TTG CAG CCT ACG GAT	702
Gln Val Gln Ala Thr Val Leu Thr Tyr Pro Asp Leu Gln Pro Thr Asp	
170 175 180	
AGA GCA ACT ATT TAC GTT AAA TCA AAA TTA GAC AAG CTT ATT TGG CAA	750
Arg Ala Thr Ile Tyr Val Lys Ser Lys Leu Asp Lys Leu Ile Trp Gln	
185 190 195	
ACA AGA ATT ACC AGA GAT CAA AAA GTT CTT AAT GTA AAG AGT TTT GAA	798
Thr Arg Ile Thr Arg Asp Gln Lys Val Leu Asn Val Lys Ser Phe Glu	
200 205 210	
GTT TAT CAT CAA TTA AAT AAA GCT ATC ACA CAT GCA GTA GGT GTA CAA	846
Val Tyr His Gln Leu Asn Lys Ala Ile Thr His Ala Val Gly Val Gln	
215 220 225 230	
TTA AAT CCA ACT GTA ACA GTT GCA CAA GTT GAC CAA GAA ATC AAA GTG	894
Leu Asn Pro Thr Val Thr Val Ala Gln Val Asp Gln Glu Ile Lys Val	
235 240 245	
CTA CAA GAA GCA TTA AAT ACT GCT CTA CAG TAAGGTAGAG ATTGAATTGA	944
Leu Gln Glu Ala Leu Asn Thr Ala Leu Gln	
250 255	
CGTATTAAAA AGGACTGGAA TTTATTAATT TCAGTCCTTT AGAATTTTA TTTAGCTGAT	1004
TTACTTGTG AAGAGATTG GTGGAAAATC AAGTACCATA CTTCATTCT CCTCCAAATA	1064
CTTGTATGTC GATTCCCTTC TAAAACATAG CTAATTAGTT TAGTTTCTG GCTAATAGAT	1124
TGTACATGAA ATTGTTCAA ATTACTAGGG TAAAAGGTTT TTCTTTTAT AAATTCATCA	1184
TGACTAT	1191

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 256 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Phe Lys Lys Leu Leu Tyr Leu Thr Gly Ser Ile Ala Gly Ile
1 5 10 15

Thr Leu Phe Ser Pro Ile Leu Thr Ser Val Gln Ala Asn Gln Ile Asn
20 25 30

Val Ser Gln Pro Ser Asn Asn Glu Ser Asn Val Ile Ser Gln Lys Lys
35 40 45

Glu Glu Ile Asp Asn Ser Leu Asn Gln Glu Ser Ala Gln Leu Tyr Ala
50 55 60

Leu Lys Glu Asp Val Lys Gly Thr Clu Lys Glu Gln Ser Val Asn Ser
65 70 75 80

Ala Ile Ser Ala Val Glu Asn Leu Lys Thr Ser Leu Arg Ala Asn Pro
85 90 95

Glu Thr Ile Tyr Asp Leu Asn Ser Ile Gly Thr Arg Val Glu Ala Ile
100 105 110

Ser Asp Val Ile Gln Ala Ile Val Phe Ser Thr Gln Gln Leu Thr Asn
115 120 125

Lys Val Asp Gln Ala His Ile Asp Met Gly Phe Ala Ile Thr Lys Leu
130 135 140

Leu Ile Arg Ile Ala Asp Pro Phe Ala Ser Asn Glu Ser Ile Lys Gly
145 150 155 160

Gln Val Glu Ala Val Lys Gln Val Gln Ala Thr Val Leu Thr Tyr Pro
165 170 175

Asp Leu Gln Pro Thr Asp Arg Ala Thr Ile Tyr Val Lys Ser Lys Leu
180 185 190

Asp Lys Leu Ile Trp Gln Thr Arg Ile Thr Arg Asp Gln Lys Val Leu
195 200 205

Asn Val Lys Ser Phe Glu Val Tyr His Gln Leu Asn Lys Ala Ile Thr
210 215 220

His Ala Val Gly Val Gln Leu Asn Pro Thr Val Thr Val Ala Gln Val
225 230 235 240

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Glu	Phe	Lys	Lys	Leu	Leu	Tyr	Leu	Thr	Gly	Ser	Ile	Ala	Gly	Ile
1				5					10					15	
Thr	Leu	Phe	Ser	Pro	Ile	Leu	Thr	Ser	Val	Gln	Ala	Asn	Gln	Ile	Asn
				20				25					30		
Val	Ser	Gln	Pro	Ser	Asn	Asn	Glu	Ser	Asn	Val	Ile	Ser	Gln	Lys	Lys
					35			40				45			
Glu	Glu	Ile	Asp	Asn	Ser	Leu	Asn	Gln	Glu	Ser	Ala	Gln	Leu	Tyr	Ala
					50		55				60				
Leu	Lys	Glu	Asp	Val	Lys	Gly	Thr	Glu	Lys	Glu	Gln	Ser	Val	Asn	Ser
					65		70		75					80	
Ala	Ile	Ser	Ala	Val	Glu	Asn	Leu	Lys	Thr	Ser	Leu	Arg	Ala	Asn	Pro
					85				90				95		
Glu	Thr	Ile	Tyr	Asp	Leu	Asn	Ser	Ile	Gly	Thr	Arg	Val	Glu	Ala	Ile
					100			105				110			
Ser	Asp	Val	Ile	Gln	Ala	Ile	Val	Phe	Ser	Thr	Gln	Gln	Leu	Thr	Asn
					115			120			125				
Lys	Val	Asp	Gln	Ala	His	Ile	Asp	Met	Gly	Phe	Ala	Ile	Thr	Lys	Leu
						130		135			140				
Leu	Ile	Arg	Ile	Ala	Asp	Pro	Phe	Ala	Ser	Asn	Glu	Ser	Ile	Lys	Gly
						145		150		155				160	
Gln	Val	Glu	Ala	Val	Lys	Gln	Val	Gln	Ala	Thr	Val	Leu	Thr	Tyr	Pro

Asp Lys Leu Ile Trp Gln Thr Arg Ile Thr Arg Asp Gln Lys Val Leu
195 200 205

Asn Val Lys Ser Phe Glu Val Tyr His Gln Leu Asn Lys Ala Ile Thr
210 215 220

His Ala Val Gly Val Gln Leu Asn Pro Thr Val Thr Val Ala Gln Val
225 230 235 240

Asp Gln Glu Ile Lys Val Leu Gln Glu Ala Leu Asn Thr Ala Leu Gln
245 250 255

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 226 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Asp Gln Val Thr Thr Pro Gln Val Val Asn His Val Asn Ser Asn Asn
1 5 10 15

Gln Ala Gln Gln Met Ala Gln Lys Leu Asp Gln Asp Ser Ile Gln Leu
20 25 30

Arg Asn Ile Lys Asp Asn Val Gln Gly Thr Asp Tyr Glu Lys Pro Val
35 40 45

Asn Glu Ala Ile Thr Ser Val Glu Lys Leu Lys Thr Ser Leu Arg Ala
50 55 60

Asn Ser Glu Thr Val Tyr Asp Leu Asn Ser Ile Gly Ser Arg Val Glu
65 70 75 80

Ala Leu Thr Asp Val Ile Glu Ala Ile Thr Phe Ser Thr Gln His Leu
85 90 95

Lys Leu Val Ile Asp Asn Ser Ile Val Asn Ser Ile Asp Val Ile Asn
115 120 125

Lys Ala Gln Val Asn Asp Val Lys Ala Leu Glu Gln Lys Val Leu Thr
130 135 140

Tyr Pro Asp Leu Lys Pro Thr Asp Arg Ala Thr Ile Tyr Thr Lys Ser
145 150 155 160

Lys Leu Asp Lys Glu Ile Trp Asn Thr Arg Phe Thr Arg Asp Lys Lys
165 170 175

Val Leu Asn Val Lys Glu Phe Lys Val Tyr Asn Thr Leu Asn Lys Ala
180 185 190

Ile Thr His Ala Val Gly Val Gln Leu Asn Pro Asn Val Thr Val Gln
195 200 205

Gln Val Asp Gln Glu Ile Val Thr Leu Gln Ala Ala Leu Gln Thr Ala
210 215 220

Leu Lys
225